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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: markspencer

Timestamp: Wed Jun 27 07:06:46 EDT 2007

=====

Application No: 10590457

Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-21 12:02:59.623

Finished: 2007-06-21 12:03:29.347

Elapsed: 0 hr(s) 0 min(s) 29 sec(s) 724 ms

Total Warnings: 116

Total Errors: 598

No. of SeqIDs Defined: 255

Actual SeqID Count: 255

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 300	Invalid codon found Leu SEQID (5) POS: 96
E 300	Invalid codon found Ser SEQID (5) POS: 100
E 300	Invalid codon found Ser SEQID (5) POS: 104
E 300	Invalid codon found Leu SEQID (5) POS: 108
E 300	Invalid codon found Lys SEQID (5) POS: 112
E 300	Invalid codon found Gly SEQID (5) POS: 116
E 300	Invalid codon found Glu SEQID (5) POS: 120
E 300	Invalid codon found Glu SEQID (5) POS: 124
E 300	Invalid codon found Val SEQID (5) POS: 128
E 300	Invalid codon found Cys SEQID (5) POS: 132
E 300	Invalid codon found Ile SEQID (5) POS: 136
E 300	Invalid codon found Asp SEQID (5) POS: 140
E 300	Invalid codon found Gly SEQID (5) POS: 144
E 300	Invalid codon found Ile SEQID (5) POS: 148
E 300	Invalid codon found Ile SEQID (5) POS: 152
E 300	Invalid codon found Tyr SEQID (5) POS: 156
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)

Input Set:

Output Set :

```
Started: 2007-06-21 12:02:59.623
```

**Finished:** 2007-06-21 12:03:29.347

**Elapsed:** 0 hr(s) 0 min(s) 29 sec(s) 724 ms

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[illegible]

**Input Set:**

**Output Set:**

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**Finished:** 2007-06-21 12:03:29.347  
**Elapsed:** 0 hr(s) 0 min(s) 29 sec(s) 724 ms  
**Total Warnings:** 116  
**Total Errors:** 598  
**No. of SeqIDs Defined:** 255  
**Actual SeqID Count:** 255

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (34)

**Input Set:**

**Output Set:**

**Started:** 2007-06-21 12:02:59.623  
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**Elapsed:** 0 hr(s) 0 min(s) 29 sec(s) 724 ms  
**Total Warnings:** 116  
**Total Errors:** 598  
**No. of SeqIDs Defined:** 255  
**Actual SeqID Count:** 255

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (40)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (42)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (44)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (50)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (64)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (82) POS (160)
W 213	Artificial or Unknown found in <213> in SEQ ID (115)
W 213	Artificial or Unknown found in <213> in SEQ ID (116)
W 213	Artificial or Unknown found in <213> in SEQ ID (121)
W 213	Artificial or Unknown found in <213> in SEQ ID (122)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)

**Input Set:**

**Output Set:**

**Started:** 2007-06-21 12:02:59.623  
**Finished:** 2007-06-21 12:03:29.347  
**Elapsed:** 0 hr(s) 0 min(s) 29 sec(s) 724 ms  
**Total Warnings:** 116  
**Total Errors:** 598  
**No. of SeqIDs Defined:** 255  
**Actual SeqID Count:** 255

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
W 213	Artificial or Unknown found in <213> in SEQ ID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (126)
W 213	Artificial or Unknown found in <213> in SEQ ID (127)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129)
W 213	Artificial or Unknown found in <213> in SEQ ID (130)
W 213	Artificial or Unknown found in <213> in SEQ ID (139)
W 213	Artificial or Unknown found in <213> in SEQ ID (140)
W 213	Artificial or Unknown found in <213> in SEQ ID (141)
W 213	Artificial or Unknown found in <213> in SEQ ID (143)
W 213	Artificial or Unknown found in <213> in SEQ ID (144)
W 213	Artificial or Unknown found in <213> in SEQ ID (145)
W 213	Artificial or Unknown found in <213> in SEQ ID (146)
W 213	Artificial or Unknown found in <213> in SEQ ID (147) This error has occurred more than 20 times, will not be displayed
E 224	<220>, <223> section required as <213> has Artificial sequence or Unknown in SEQID (187)

# SEQUENCE LISTING

<110> Cirpus, Petra  
 Bauer, Jorg  
 Qiu, Xiao  
 Wu, Guohai  
 Datla, Nagamani

<120> METHOD FOR PRODUCING POLYUNSATURATED FATTY ACIDS IN TRANSGENIC  
 PLANTS

<130> 13987-00020-US

<140> 10590457  
 <141> 2007-06-21

<150> 10/590,457  
 <151> 2006-08-25

<150> PCT/EP2005/001863  
 <151> 2005-02-23

<150> DE 10 2004 009 457.8  
 <151> 2004-02-27

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 <151> 2004-03-13

<150> DE 10 2004 017 518.7  
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<150> DE 10 2004 024 014.0  
 <151> 2004-05-14

<150> PCT/EP2004/07957  
 <151> 2004-07-16

<150> DE 10 2004 062 543.3  
 <151> 2004-12-24

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<170> PatentIn version 3.4

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 <223> Delta-8 desaturase

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1				5					10					15			

  

tat	gat	gtg	tct	gcc	tgg	gtc	aat	ttc	cac	cct	ggt	ggt	gcg	gaa	att		96
Tyr	Asp	Val	Ser	Ala	Trp	Val	Asn	Phe	His	Pro	Gly	Gly	Ala	Glu	Ile		
			20					25					30				

  

ata	gag	aat	tac	caa	gga	agg	gat	gcc	act	gat	gcc	ttc	atg	gtt	atg		144
Ile	Glu	Asn	Tyr	Gln	Gly	Arg	Asp	Ala	Thr	Asp	Ala	Phe	Met	Val	Met		
		35						40				45					

  

cac	tct	caa	gaa	gcc	ttc	gac	aag	ctc	aag	cgc	atg	ccc	aaa	atc	aat		192
His	Ser	Gln	Glu	Ala	Phe	Asp	Lys	Leu	Lys	Arg	Met	Pro	Lys	Ile	Asn		
		50					55				60						

  

ccc	agt	tct	gag	ttg	cca	ccc	cag	gct	gca	gtg	aat	gaa	gct	caa	gag		240
Pro	Ser	Ser	Glu	Leu	Pro	Pro	Gln	Ala	Ala	Val	Asn	Glu	Ala	Gln	Glu		
65					70					75					80		

  

gat	ttc	cgg	aag	ctc	cga	gaa	gag	ttg	atc	gca	act	ggc	atg	ttt	gat		288
Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp		
				85					90					95			

  

gcc	tcc	ccc	ctc	tgg	tac	tca	tac	aaa	atc	agc	acc	aca	ctg	ggc	ctt		336
Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu		
			100						105					110			

  

gga	gtg	ctg	ggt	tat	ttc	ctg	atg	gtt	cag	tat	cag	atg	tat	ttc	att		384
Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile		
		115					120					125					

  

ggg	gca	gtg	ttg	ctt	ggg	atg	cac	tat	caa	cag	atg	ggc	tgg	ctt	tct		432
Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser		
		130				135						140					

  

cat	gac	att	tgc	cac	cac	cag	act	ttc	aag	aac	cgg	aac	tgg	aac	aac		480
His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn		
145					150					155					160		

  

ctc	gtg	gga	ctg	gta	ttt	ggc	aat	ggt	ctg	caa	ggt	ttt	tcc	gtg	aca		528
Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr		
			165						170					175			

  

tgc	tgg	aag	gac	aga	cac	aat	gca	cat	cat	tcg	gca	acc	aat	gtt	caa		576
Cys	Trp	Lys	Asp	Arg	His	Asn	Ala	His	His	Ser	Ala	Thr	Asn	Val	Gln		
			180					185					190				

  

ggg	cac	gac	cct	gat	att	gac	aac	ctc	ccc	ctc	tta	gcc	tgg	tct	gag		624
Gly	His	Asp	Pro	Asp	Ile	Asp	Asn	Leu	Pro	Leu	Leu	Ala	Trp	Ser	Glu		
		195					200					205					

  

gat	gac	gtc	aca	cgg	gcg	tca	ccg	att	tcc	cgc	aag	ctc	att	cag	ttc		672
Asp	Asp	Val	Thr	Arg	Ala	Ser	Pro	Ile	Ser	Arg	Lys	Leu	Ile	Gln	Phe		



210	215	220	
cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg			720
Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp			
225	230	235	240
tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac			768
Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn			
	245	250	255
caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg			816
Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu			
	260	265	270
cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc			864
His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile			
	275	280	285
ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc			912
Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe			
	290	295	300
ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc			960
Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile			
305	310	315	320
ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat			1008
Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His			
	325	330	335
gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga			1056
Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly			
	340	345	350
ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc			1104
Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg			
	355	360	365
cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag			1152
His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys			
	370	375	380
cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc			1200
His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile			
385	390	395	400
ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc			1248
Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro			
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gcg ggg aag gct cta taa			1266
Ala Gly Lys Ala Leu			
	420		

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<211> 421

<212> PRT

<213> *Euglena gracilis*

<400> 2

Met	Lys	Ser	Lys	Arg	Gln	Ala	Leu	Pro	Leu	Thr	Ile	Asp	Gly	Thr	Thr
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Tyr	Asp	Val	Ser	Ala	Trp	Val	Asn	Phe	His	Pro	Gly	Gly	Ala	Glu	Ile
			20					25					30		

Ile	Glu	Asn	Tyr	Gln	Gly	Arg	Asp	Ala	Thr	Asp	Ala	Phe	Met	Val	Met
		35					40					45			

His	Ser	Gln	Glu	Ala	Phe	Asp	Lys	Leu	Lys	Arg	Met	Pro	Lys	Ile	Asn
	50						55				60				

Pro	Ser	Ser	Glu	Leu	Pro	Pro	Gln	Ala	Ala	Val	Asn	Glu	Ala	Gln	Glu
65					70					75					80

Asp	Phe	Arg	Lys	Leu	Arg	Glu	Glu	Leu	Ile	Ala	Thr	Gly	Met	Phe	Asp
			85						90					95	

Ala	Ser	Pro	Leu	Trp	Tyr	Ser	Tyr	Lys	Ile	Ser	Thr	Thr	Leu	Gly	Leu
			100					105						110	

Gly	Val	Leu	Gly	Tyr	Phe	Leu	Met	Val	Gln	Tyr	Gln	Met	Tyr	Phe	Ile
		115					120					125			

Gly	Ala	Val	Leu	Leu	Gly	Met	His	Tyr	Gln	Gln	Met	Gly	Trp	Leu	Ser
	130					135					140				

His	Asp	Ile	Cys	His	His	Gln	Thr	Phe	Lys	Asn	Arg	Asn	Trp	Asn	Asn
145					150					155					160

Leu	Val	Gly	Leu	Val	Phe	Gly	Asn	Gly	Leu	Gln	Gly	Phe	Ser	Val	Thr
			165						170					175	

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln  
180 185 190

Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu  
195 200 205

Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe  
210 215 220

Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp  
225 230 235 240

Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn  
245 250 255

Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu  
260 265 270

His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile  
275 280 285

Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe  
290 295 300

Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile  
305 310 315 320

Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His  
325 330 335

Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly  
340 345 350

Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg  
355 360 365

His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys  
370 375 380

His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile  
385 390 395 400

Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro

Ala Gly Lys Ala Leu  
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<211> 777

<212> DNA

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<220>

<221> CDS

<222> (1)..(777)

<223> Delta-9 elongase

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1 5 10 15	

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg	96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro	
20 25 30	

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg	144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg	
35 40 45	

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg	192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu	
50 55 60	

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc	240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly	
65 70 75 80	

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag	288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln	
85 90 95	

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag	336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys	
100 105 110	

gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg	384
Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu	
115 120 125	
agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat	432
Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp	
130 135 140	
gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg	480
Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met	
145 150 155 160	
ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc	528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu	
165 170 175	
acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg	576
Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met	
180 185 190	
cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc	624
Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile	
195 200 205	
aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct	672
Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala	
210 215 220	
ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt	720
Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe	
225 230 235 240	
ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag	768
Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys	
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cag ctc tag	777
Gln Leu	

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<211> 258

<212> PRT

<213> Isochrysis galbana

<400> 4

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20 25 30

Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg  
35 40 45

Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu  
50 55 60

Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly  
65 70 75 80

Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln  
85 90 95

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys  
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu  
115 120 125

Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp  
130 135 140

Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met  
145 150 155 160

Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu  
165 170 175

Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met  
180 185 190

Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile  
195 200 205

Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala  
210 215 220

Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe  
225 230 235 240

Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys  
245 250 255

Gln Leu

<210> 5

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<212> DNA

<213> *Phaeodactylum tricornutum*

<220>

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<223> Delta-5 desaturase

<400> 5

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Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val	
1 5 10 15	

gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt	96
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser	
20 25 30	

ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat	144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr	
35 40 45	

gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt	192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe	
50 55 60	

ggg ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat	240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His	
65 70 75 80	